

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/585,717  
Source: TEBP  
Date Processed by STIC: 7/19/06

# ***ENTERED***



IFWP

**RAW SEQUENCE LISTING**

DATE: 07/19/2006

PATENT APPLICATION: US/10/585,717

TIME: 08:32:42

Input Set : A:\211010048U2.txt

Output Set: N:\CRF4\07192006\J585717.raw

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3 <110> APPLICANT: Leppert, Mark F.
4     Singh, Nanda A.
6 <120> TITLE OF INVENTION: Mutant Sodium Channel Nav1.7 and Methods
7     Related Thereto
9 <130> FILE REFERENCE: 21101.0048U2
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/585,717
C--> 11 <141> CURRENT FILING DATE: 2006-07-11
11 <150> PRIOR APPLICATION NUMBER: PCT/US05/02059
12 <151> PRIOR FILING DATE: 2005-01-21
14 <150> PRIOR APPLICATION NUMBER: 60/538,149
15 <151> PRIOR FILING DATE: 2004-01-21
17 <160> NUMBER OF SEQ ID NOS: 38
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 5934
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
28     synthetic construct
30 <400> SEQUENCE: 1
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33 gatgatgatg aagaagcccc aaagccaagc agtgacttgg aagctggcaa acaactgccc 180
34 ttcattctatg gggacattcc tcccggcatg gtgtcagagc ccctggagga cttggacccc 240
35 tactatgcag acaaaaagac tttcatagta ttgaacaaag ggaaaacaat cttccgtttc 300
36 aatgccacac ctgctttata tatgctttct cctttcagtc ctctaagaag aatatctatt 360
37 aagatttttag tacactcctt attcagcatg ctcatcatgt gcaactattc gacaaactgc 420
38 atattttatga ccatgaataa cccgccggac tggaccaaaa atgtcgagta cacttttact 480
39 ggaatatata cttttgaatc acttgtaaaa atccttgcaa gaggtctctg tgtaggagaa 540
40 ttcacttttc ttcgtgaccc gtggaactgg ctggattttg tcgtcattgt ttttgcgat 600
41 ttaacagaat ttgtaaacct aggcaatgtt tcagctcttc gaactttcag agtattgaga 660
42 gctttgaaaa ctatttctgt aatcccaggc ctgaagacaa ttgtaggggc tttgatccag 720
43 tcagtgaaga agctttctga tgtcatgatc ctgactgtgt tctgtctgag tgtgtttgca 780
44 ctaattggac tacagctgtt catgggaaac ctgaagcata aatgttttcg aaattcactt 840
45 gaaaataatg aaacattaga aagcataatg aataccctag agagtgaaga agactttaga 900
46 aaatattttt attacttgga aggatccaaa gatgctctcc tttgtggttt cagcacagat 960
47 tcaggctcagt gtccagaggg gtacacctgt gtgaaaattg gcagaaaccc tgattatggc 1020
48 tacacgagct ttgacacttt cagctgggcc ttcttagcct tgtttaggct aatgacccaa 1080
49 gattactggg aaaaccttta ccaacagacg ctgcgtgctg ctggcaaac ctacatgatc 1140
50 ttctttgtcg tagtgatttt cctgggctcc ttttatctaa taaacttgat cctggctgtg 1200
51 gttgccatgg catatgaaga acagaaccag gcaaacattg aagaagctaa acagaaagaa 1260
52 ttagaatttc aacagatgtt agaccgtctt aaaaaagagc aagaagaagc tgaggcaatt 1320

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53 gcagcggcag cggctgaata tacaagtatt aggagaagca gaattatggg cctctcagag 1380
54 agttcttctg aaacatccaa actgagctct aaaagtgcga aagaaagaag aaacagaaga 1440
55 aagaaaaaga atcaaaagaa gctctccagt ggagaggaaa agggagatgc tgagaaattg 1500
56 tcgaaatcag aatcagagga cagcatcaga agaaaaagtt tccaccttgg tgtcgaagg 1560
57 cataggcgag cacatgaaaa gaggttgtct accccaatc agtcaccact cagcattcgt 1620
58 ggctccttgt tttctgcaag gcgaagcagc agaacaagtc tttttagttt caaaggcaga 1680
59 ggaagagata taggatctga gactgaattt gccgatgatg agcacagcat ttttgagac 1740
60 aatgagagca gaaggggctc actgtttgtg cccacagac cccaggagcg acgcagcagt 1800
61 aacatcagcc aagccagtag gtccccacca atgctgccgg tgaacgggaa aatgcacagt 1860
62 gctgtggact gcaacgggtg ggtctccctg gttgatggac gctcagccct catgctcccc 1920
63 aatggacagc ttctgccaga gggcagcacc aatcaaatac acaagaaaag gcgttgtagt 1980
64 tctatctcc ttccagagga tatgctgaat gatcccaacc tcagacagag agcaatgagt 2040
65 agagcaagca tattaacaaa cactgtggaa gaacttgaag agtccagaca aaaatgtcca 2100
66 ccttggtggt acagatttgc acacaaattc ttgatctgga attgctctcc atattggata 2160
67 aaattcaaaa agtgtatcta ttttattgta atggatcctt ttgtagatct tgcaattacc 2220
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69 ttcaaaaatg tacttgctat aggaaatttg gtctttactg gaatctttgc agctgaaatg 2340
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102 tacatgtata tttatattgt cgtctttatc atctttgggt cattcttcac tttgaacttg 4320
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105 aagccacaaa agccaattcc tcgaccaggg aacaaaatcc aaggatgtat atttgacct 4500
106 gtgacaaatc aagcctttga tattagtatc atggttctta tctgtctcaa catggtaacc 4560
107 atgatggtag aaaaggaggg tcaaagtcaa catatgactg aagttttata ttggataaat 4620
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116 ccaccgact gtgacccaaa aaaagttcat cctggaagtt cagttgaagg agactgtggt 5160
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128 accacctctc caccttcata tgatagtgtg acaaagccag acaaagagaa atatgaacaa 5880
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131 &lt;210&gt; SEQ ID NO: 2

132 &lt;211&gt; LENGTH: 1977

133 &lt;212&gt; TYPE: PRT

134 &lt;213&gt; ORGANISM: Homo Sapien

137 &lt;400&gt; SEQUENCE: 2

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139 1 5 10 15
140 Lys Gln Ser Leu Ala Leu Ile Glu Gln Arg Ile Ala Glu Arg Lys Ser
141 20 25 30
142 Lys Glu Pro Lys Glu Glu Lys Lys Asp Asp Asp Glu Glu Ala Pro Lys
143 35 40 45
144 Pro Ser Ser Asp Leu Glu Ala Gly Lys Gln Leu Pro Phe Val Tyr Gly
145 50 55 60
146 Asp Ile Pro Pro Gly Met Val Ser Glu Pro Leu Glu Asp Leu Asp Pro
147 65 70 75 80
148 Tyr Tyr Ala Asp Lys Lys Thr Phe Ile Val Leu Asn Lys Gly Lys Thr
149 85 90 95
150 Ile Phe Arg Phe Asn Ala Thr Pro Ala Leu Tyr Met Leu Ser Pro Phe
151 100 105 110
152 Ser Pro Leu Arg Arg Ile Ser Ile Lys Ile Leu Val His Ser Leu Phe
153 115 120 125

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154 Ser Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Ile Phe Met Thr
155      130      135      140
156 Met Asn Asn Pro Pro Asp Trp Thr Lys Asn Val Glu Tyr Thr Phe Thr
157 145      150      155      160
158 Gly Ile Tyr Thr Phe Glu Ser Leu Val Lys Ile Leu Ala Arg Gly Phe
159      165      170      175
160 Cys Val Gly Glu Phe Thr Phe Leu Arg Asp Pro Trp Asn Trp Leu Asp
161      180      185      190
162 Phe Val Val Ile Val Phe Ala Tyr Leu Thr Glu Phe Val Asn Leu Gly
163      195      200      205
164 Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys Thr
165      210      215      220
166 Ile Ser Val Ile Pro Gly Leu Lys Thr Ile Val Gly Ala Leu Ile Gln
167 225      230      235      240
168 Ser Val Lys Lys Leu Ser Asp Val Met Ile Leu Thr Val Phe Cys Leu
169      245      250      255
170 Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe Met Gly Asn Leu Lys
171      260      265      270
172 His Lys Cys Phe Arg Asn Ser Leu Glu Asn Asn Glu Thr Leu Glu Ser
173      275      280      285
174 Ile Met Asn Thr Leu Glu Ser Glu Glu Asp Phe Arg Lys Tyr Phe Tyr
175      290      295      300
176 Tyr Leu Glu Gly Ser Lys Asp Ala Leu Leu Cys Gly Phe Ser Thr Asp
177 305      310      315      320
178 Ser Gly Gln Cys Pro Glu Gly Tyr Thr Cys Val Lys Ile Gly Arg Asn
179      325      330      335
180 Pro Asp Tyr Gly Tyr Thr Ser Phe Asp Thr Phe Ser Trp Ala Phe Leu
181      340      345      350
182 Ala Leu Phe Arg Leu Met Thr Gln Asp Tyr Trp Glu Asn Leu Tyr Gln
183      355      360      365
184 Gln Thr Leu Arg Ala Ala Gly Lys Thr Tyr Met Ile Phe Phe Val Val
185      370      375      380
186 Val Ile Phe Leu Gly Ser Phe Tyr Leu Ile Asn Leu Ile Leu Ala Val
187 385      390      395      400
188 Val Ala Met Ala Tyr Glu Glu Gln Asn Gln Ala Asn Ile Glu Glu Ala
189      405      410      415
190 Lys Gln Lys Glu Leu Glu Phe Gln Gln Met Leu Asp Arg Leu Lys Lys
191      420      425      430
192 Glu Gln Glu Glu Ala Glu Ala Ile Ala Ala Ala Ala Glu Tyr Thr
193      435      440      445
194 Ser Ile Arg Arg Ser Arg Ile Met Gly Leu Ser Glu Ser Ser Ser Glu
195      450      455      460
196 Thr Ser Lys Leu Ser Ser Lys Ser Ala Lys Glu Arg Arg Asn Arg Arg
197 465      470      475      480
198 Lys Lys Lys Asn Gln Lys Lys Leu Ser Ser Gly Glu Glu Lys Gly Asp
199      485      490      495
200 Ala Glu Lys Leu Ser Lys Ser Glu Ser Glu Asp Ser Ile Arg Arg Lys
201      500      505      510
202 Ser Phe His Leu Gly Val Glu Gly His Arg Arg Ala His Glu Lys Arg

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203		515		520		525										
204	Leu	Ser	Thr	Pro	Asn	Gln	Ser	Pro	Leu	Ser	Ile	Arg	Gly	Ser	Leu	Phe
205		530					535					540				
206	Ser	Ala	Arg	Arg	Ser	Ser	Arg	Thr	Ser	Leu	Phe	Ser	Phe	Lys	Gly	Arg
207	545					550					555				560	
208	Gly	Arg	Asp	Ile	Gly	Ser	Glu	Thr	Glu	Phe	Ala	Asp	Asp	Glu	His	Ser
209					565					570				575		
210	Ile	Phe	Gly	Asp	Asn	Glu	Ser	Arg	Arg	Gly	Ser	Leu	Phe	Val	Pro	His
211				580					585				590			
212	Arg	Pro	Gln	Glu	Arg	Arg	Ser	Ser	Asn	Ile	Ser	Gln	Ala	Ser	Arg	Ser
213			595				600					605				
214	Pro	Pro	Met	Leu	Pro	Val	Asn	Gly	Lys	Met	His	Ser	Ala	Val	Asp	Cys
215		610					615					620				
216	Asn	Gly	Val	Val	Ser	Leu	Val	Asp	Gly	Arg	Ser	Ala	Leu	Met	Leu	Pro
217	625					630					635				640	
218	Asn	Gly	Gln	Leu	Leu	Pro	Glu	Gly	Thr	Thr	Asn	Gln	Ile	His	Lys	Lys
219				645					650					655		
220	Arg	Arg	Cys	Ser	Ser	Tyr	Leu	Leu	Ser	Glu	Asp	Met	Leu	Asn	Asp	Pro
221				660					665				670			
222	Asn	Leu	Arg	Gln	Arg	Ala	Met	Ser	Arg	Ala	Ser	Ile	Leu	Thr	Asn	Thr
223			675				680					685				
224	Val	Glu	Glu	Leu	Glu	Glu	Ser	Arg	Gln	Lys	Cys	Pro	Pro	Trp	Trp	Tyr
225		690					695					700				
226	Arg	Phe	Ala	His	Lys	Phe	Leu	Ile	Trp	Asn	Cys	Ser	Pro	Tyr	Trp	Ile
227	705				710				715						720	
228	Lys	Phe	Lys	Lys	Cys	Ile	Tyr	Phe	Ile	Val	Met	Asp	Pro	Phe	Val	Asp
229				725					730					735		
230	Leu	Ala	Ile	Thr	Ile	Cys	Ile	Val	Leu	Asn	Thr	Leu	Phe	Met	Ala	Met
231				740					745				750			
232	Glu	His	His	Pro	Met	Thr	Glu	Glu	Phe	Lys	Asn	Val	Leu	Ala	Ile	Gly
233			755				760					765				
234	Asn	Leu	Val	Phe	Thr	Gly	Ile	Phe	Ala	Ala	Glu	Met	Val	Leu	Lys	Leu
235		770				775					780					
236	Ile	Ala	Met	Asp	Pro	Tyr	Glu	Tyr	Phe	Gln	Val	Gly	Trp	Asn	Ile	Phe
237	785					790					795				800	
238	Asp	Ser	Leu	Ile	Val	Thr	Leu	Ser	Leu	Val	Glu	Leu	Phe	Leu	Ala	Asp
239				805					810					815		
240	Val	Glu	Gly	Leu	Ser	Val	Leu	Arg	Ser	Phe	Arg	Leu	Leu	Arg	Val	Phe
241				820					825				830			
242	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	Asn	Met	Leu	Ile	Lys	Ile	Ile
243			835				840					845				
244	Gly	Asn	Ser	Val	Gly	Ala	Leu	Gly	Asn	Leu	Thr	Leu	Val	Leu	Ala	Ile
245		850				855					860					
246	Ile	Val	Phe	Ile	Phe	Ala	Val	Val	Gly	Met	Gln	Leu	Phe	Gly	Lys	Ser
247	865				870						875				880	
248	Tyr	Lys	Glu	Cys	Val	Cys	Lys	Ile	Asn	Asp	Cys	Thr	Leu	Pro	Arg	
249				885					890					895		
250	Trp	His	Met	Asn	Asp	Phe	Phe	His	Ser	Phe	Leu	Ile	Val	Phe	Arg	Val
251				900					905				910			

**VERIFICATION SUMMARY**

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date